RAW SEQUENCE LISTING
PATENT APPLICATION **US/09/377,675**

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> This Raw Listing contains the General Information
> Section and up to first 5 pages.

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 1   <110> APPLICANT: Olwin, Bradley B.
 2         Rosenthal, Richard S.
 3   <120> TITLE OF INVENTION: CHIMERIC FIBROBLAST GROWTH FACTOR PROTEINS, NUCLEIC
 4         ACID MOLECULES, AND USES THEREOF
 5   <130> FILE REFERENCE: 2848-32
 6   <140> CURRENT APPLICATION NUMBER: US/09/377,675
 7   <141> CURRENT FILING DATE: 1999-08-19
 8   <150> EARLIER APPLICATION NUMBER: 60/097,160
 9   <151> EARLIER FILING DATE: 1998-08-19
10   <160> NUMBER OF SEQ ID NOS: 27
11   <170> SOFTWARE: PatentIn Ver. 2.0
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14   <212> TYPE: DNA
15   <213> ORGANISM: chimeric sequence
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23         tgg aaa aag gcg gct gct ggt tct atc act acc ctg cca gct ctg cca    97
24         Trp Lys Lys Ala Ala Ala Gly Ser Ile Thr Thr Leu Pro Ala Leu Pro
25          15              20              25                      30
26         gaa gac ggt ggt tct ggt gcc ttc cca cca ggt cac ttc aaa gac cca   145
27         Glu Asp Gly Gly Ser Gly Ala Phe Pro Pro Gly His Phe Lys Asp Pro
28                          35              40                      45
29         aaa cgt ctg tac tgc aaa aac ggt ggt ttc ttc ctg cgc atc cac ccc   193
30         Lys Arg Leu Tyr Cys Lys Asn Gly Gly Phe Phe Leu Arg Ile His Pro
31                      50                  55                  60
32         gac ggc cga gtg gac ggg gtc cgc gag aag agc gac cca cac atc aaa   241
33         Asp Gly Arg Val Asp Gly Val Arg Glu Lys Ser Asp Pro His Ile Lys
34                      65                  70                  75
35         cta caa ctt caa gca gaa gag aga ggg gtt gtg tct atc aaa gga gtg   289
36         Leu Gln Leu Gln Ala Glu Glu Arg Gly Val Val Ser Ile Lys Gly Val
37                  80                  85                  90
38         tgt gca aac cgt tac ctt gct atg aaa gaa gat gga aga tta cta gct   337
39         Cys Ala Asn Arg Tyr Leu Ala Met Lys Glu Asp Gly Arg Leu Leu Ala
40          95                 100                 105                 110
41         tct aaa tgt gtt aca gac gag tgt ttc ttt ttt gaa cga ttg gag tct   385
42         Ser Lys Cys Val Thr Asp Glu Cys Phe Phe Phe Glu Arg Leu Glu Ser
43                         115                 120                 125
44         aat aac tac aat act tac cgg tca agg aaa tac acc agt tgg tat gtg   433
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45              Asn Asn Tyr Asn Thr Tyr Arg Ser Arg Lys Tyr Thr Ser Trp Tyr Val
46                          130                 135                 140
47              gca ctg aaa cga act ggg cag tat aaa ctt gga tcc aaa aca gga cct    481
48              Ala Leu Lys Arg Thr Gly Gln Tyr Lys Leu Gly Ser Lys Thr Gly Pro
49                          145                 150                 155
50              ggg cag aaa gct ata ctt ttt ctt cca atg tct gct aag agc gaa cag    529
51              Gly Gln Lys Ala Ile Leu Phe Leu Pro Met Ser Ala Lys Ser Glu Gln
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64                          20                  25                  30
65              Gly Gly Ser Gly Ala Phe Pro Pro Gly His Phe Lys Asp Pro Lys Arg
66                          35                  40                  45
67              Leu Tyr Cys Lys Asn Gly Gly Phe Phe Leu Arg Ile His Pro Asp Gly
68                          50                  55                  60
69              Arg Val Asp Gly Val Arg Glu Lys Ser Asp Pro His Ile Lys Leu Gln
70                          65                  70                  75                  80
71              Leu Gln Ala Glu Glu Arg Gly Val Val Ser Ile Lys Gly Val Cys Ala
72                          85                  90                  95  .
73              Asn Arg Tyr Leu Ala Met Lys Glu Asp Gly Arg Leu Leu Ala Ser Lys
74                          100                 105                 110
75              Cys Val Thr Asp Glu Cys Phe Phe Phe Glu Arg Leu Glu Ser Asn Asn
76                          115                 120                 125
77              Tyr Asn Thr Tyr Arg Ser Arg Lys Tyr Thr Ser Trp Tyr Val Ala Leu
78                          130                 135                 140
79              Lys Arg Thr Gly Gln Tyr Lys Leu Gly Ser Lys Thr Gly Pro Gly Gln
80                          145                 150                 155                 160
81              Lys Ala Ile Leu Phe Leu Pro Met Ser Ala Lys Ser·Glu Gln Lys Leu
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88  <213> ORGANISM: chimeric sequence
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98                  15                          20                   25
99          gaa gac ggt ggt tct ggt gcc ttc cca cca ggt cac ttc aaa gac cca    145
100         Glu Asp Gly Gly Ser Gly Ala Phe Pro Pro Gly His Phe Lys Asp Pro
101                 30                          35                   40                   45
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103         Lys Arg Leu Tyr Cys Lys Asn Gly Gly Phe Phe Leu Arg Ile His Pro
104                          50                      55                   60
105         gac ggc cga gtg gac ggg gtc cgc gag aag agc gac cca cac atc aaa    241
106         Asp Gly Arg Val Asp Gly Val Arg Glu Lys Ser Asp Pro His Ile Lys
107                          65                      70                   75
108         cta caa ctt caa gca gaa gag aga ggg gtt gtg tct atc aaa gga gtg    289
109         Leu Gln Leu Gln Ala Glu Glu Arg Gly Val Val Ser Ile Lys Gly Val
110                          80                      85                   90
111         tgt gca aac cgt tac ctt gct atg aaa gaa gat gga aga tta cta gct    337
112         Cys Ala Asn Arg Tyr Leu Ala Met Lys Glu Asp Gly Arg Leu Leu Ala
113                          95                     100                  105
114         tct aaa tgt gtt aca gac gag tgt ttc ttt ttt gaa cga ttg gag tct    385
115         Ser Lys Cys Val Thr Asp Glu Cys Phe Phe Phe Glu Arg Leu Glu Ser
116         110                         115                  120                  125
117         aat aac tac aat act tac cgg tca agg aaa tac acc agt tgg tat gtg    433
118         Asn Asn Tyr Asn Thr Tyr Arg Ser Arg Lys Tyr Thr Ser Trp Tyr Val
119                          130                     135                  140
120         gca ctg aaa cga act ggg cag tat aaa ctt gga tcc aaa aca gga cct    481
121         Ala Leu Lys Arg Thr Gly Gln Tyr Lys Leu Gly Ser Lys Thr Gly Pro
122                          145                     150                  155
123         ggg cag aaa gct ata ctt ttt ctt cca atg tct gct aag agc gaa cag    529
124         Gly Gln Lys Ala Ile Leu Phe Leu Pro Met Ser Ala Lys Ser Glu Gln
125                          160                     165                  170
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128                          175                     180
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132   <213> ORGANISM: chimeric sequence
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138         Gly Ser Gly Ala Phe Pro Pro Gly His Phe Lys Asp Pro Lys Arg Leu
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140         Tyr Cys Lys Asn Gly Gly Phe Phe Leu Arg Ile His Pro Asp Gly Arg
141                          50                      55                   60
142         Val Asp Gly Val Arg Glu Lys Ser Asp Pro His Ile Lys Leu Gln Leu
143                          65                      70                   75                   80
144         Gln Ala Glu Glu Arg Gly Val Val Ser Ile Lys Gly Val Cys Ala Asn
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149                     115                 120                 125
150        Asn Thr Tyr Arg Ser Arg Lys Tyr Thr Ser Trp Tyr Val Ala Leu Lys
151                     130                 135                 140
152        Arg Thr Gly Gln Tyr Lys Leu Gly Ser Lys Thr Gly Pro Gly Gln Lys
153                     145                 150                 155                 160
154        Ala Ile Leu Phe Leu Pro Met Ser Ala Lys Ser Glu Gln Lys Leu Ile
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166                      20                  25                  30
167        Arg Ile His Pro Asp Gly Arg Val Asp Gly Val Arg Glu Lys Ser Asp
168                      35                  40                  45
169        Pro His Ile Lys Leu Gln Leu Gln Ala Glu Glu Arg Gly Val Val Ser
170                      50                  55                  60
171        Ile Lys Gly Val Cys Ala Asn Arg Tyr Leu Ala Met Lys Glu Asp Gly
172          65                  70                  75                  80
173        Arg Leu Leu Ala Ser Lys Cys Val Thr Asp Glu Cys Phe Phe Phe Glu
174                      85                  90                  95
175        Arg Leu Glu Ser Asn Asn Tyr Asn Thr Tyr Arg Ser Arg Lys Tyr Ser
176                     100                 105                 110
177        Ser Trp Tyr Val Ala Leu Lys Arg Thr Gly Gln Tyr Lys Leu Gly Pro
178                     115                 120                 125
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181        Lys Ser
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185   <212> TYPE: PRT
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191                      20                  25                  30
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194        Pro His Ile Lys Leu Gln Leu Gln Ala Glu Glu Arg Gly Val Val Ser
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200           Arg Leu Glu Ser Asn Asn Tyr Asn Thr Tyr Arg Ser Arg Lys Tyr Thr
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202           Ser Trp Tyr Val Ala Leu Lys Arg Thr Gly Gln Tyr Lys Leu Gly Ser
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206           Lys Ser
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216                  20                    25                    30
217           Gly Thr Lys Asp Arg Ser Asp Gly His Ile Gln Leu Phe Leu Cys Ala
218                  35                    40                    45
219           Glu Ser Ile Gly Glu Val Tyr Ile Lys Ser Thr Glu Thr Gly Gln Phe
220                  50                    55                    60
221           Leu Ala Met Asp Thr Asp Gly Leu Leu Tyr Gly Ser Gln Thr Pro Asp
222                  65                    70                    75                    80
223           Glu Glu Cys Leu Phe Leu Glu Arg Leu Glu Glu Asn His Tyr Asn Thr
224                                 85                    90                    95
225           Tyr Ile Ser Lys Lys His Ala Glu Lys His Trp Phe Val Gly Leu Lys
226                               100                   105                   110
227           Lys Asn Gly Arg Ser Lys Leu Glu Pro Arg Thr His Phe Gly Gln Lys
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232    <211> LENGTH: 140
233    <212> TYPE: PRT
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239                  20                    25                    30
240           Gly Thr Arg Asp Arg Ser Asp Gln His Ile Gln Leu Gln Leu Ser Ala
241                  35                    40                    45
242           Glu Ser Tyr Gly Glu Tyr Tyr Ile Lys Ser Thr Glu Thr Gly Gln Tyr
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244           Leu Ala Met Asp Thr Asp Gly Leu Leu Tyr Gly Ser Gln Thr Pro Asn
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